

REMARKS

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In response, the Examiner states (1) Applicants' asserted utility is not specific, e.g., it is applicable to any naturally occurring polypeptide and (2) Applicants' statement (in the specification) that the peptide, "because of bearing a cysteine-like domain, is considered to process a proteinase-inhibitor activity" is insufficient; in other words, the Examiner points out Applicants do not assert the protein has any demonstrated function. Those points are addressed in turn.

As noted, the claims are rejected under 35 U.S.C. § 101 as not having a specific and substantial utility that is credible (USPTO Utility Examination Guidelines, 66 Fed. Reg. at 1098). In this regard, the Examiner necessarily contends (i) the activity of the

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^{2/} Regarding the Examiner's technical analyses of the unpredictable activity resulting from amino acid changes, and "sequence-to-function methods of assigning protein function" such is based on old art and is not the current position of either those of ordinary skill, or the Patent and Trademark Office. That is, while changes do occur (and some are drastic), similarity is, nevertheless, now reasonably expected, as discussed below.

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present invention is not credible since (ii) those of ordinary skill recognize protein activity cannot be predicted from known homologous sequences. According to the Examiner, implicitly at least, the pending claims do not satisfy the utility requirement of 35 USC 101 because, given the state of the art, structure-function analysis is unpredictable. This basis of rejection is, respectfully submitted, without foundation either in law or in fact.

The Examiner's point concerning the unpredictability of protein activity from known homologous sequences is not well-taken by those of ordinary skill. See, e.g., Principles of Protein Structure, Cantor, ed. (1978) 167 wherein it is explicitly taught that

“[h]omologous proteins result from speciation or differentiation. Comparisons between homologous proteins have yielded general rules for protein structures (citing Schulz, Angew. Chem. Int. Edit., Vol. 16 (1977) 23-33). . . . In this context it is often useful to distinguish between protein speciation and protein differentiation (citing Molecular evolution and Polymorphism, Kimura ed. (1977) National Institute of Genetics, Mishima, Japan). Speciation is the evolution of homologous proteins possessing a common function in different organisms.”

This knowledge is summarized in the art as evidencing that establishing homology between the unknown and reference proteins permits the skilled artisan to assume the unknown unexpressed protein and the known reference protein have the same function. Functional Genomics, Science, Vol. 278, No. 601 (1997).

This is not an aberrant position; similarly, the American Society of Human Genetics (“ASHG”) similarly acknowledges “sequence homology is a useful predictor of gene function.” Letter from Ronald Worton, Ph.D., President, ASHG, to the Honorable Q. Todd Dickinson, Assistant Secretary of Commerce and Commissioner of Patents and

Trademarks, United States Patent and Trademark Office at 2 (Mar. 22, 2000) (on file with the USPTO).

Additionally, the USPTO too recognizes the state of this art in Example 10 of the Utility Training Materials: DNA fragments encoding a Full Open Reading Frame (ORF). In the example the Examiner is directed not to reject the claims merely because the applicant's asserted utility is premised on the "overall level of sequence similarity between SEQ ID NO:3 [the unknown sequence] and the consensus sequence of the known DNA ligases that are presented in the specification." Indeed, Example 10 acknowledges that "homology between the known and unknown protein is sufficient to ascribe the known protein's function to the unknown; thus the claim possesses credible, substantial, and specific utility."^{3/} Id. at 54.^{4/}

Moreover, the PTO acknowledges as well utility is well-established if it is readily apparent to one skilled in the art. Id. at 55. This is in conformity with the law promulgated by the Federal Circuit, which notes 35 U.S.C. 112 can be satisfied even by "genus claims to nucleic acids based on their hybridization properties, . . . [if the subject

^{3/} Although the Examiner does not rely upon this statement because the percent homology set forth in the specification is ca. 30%, such is neither proper nor dispositive. First, the known conserved regions are homologous and second, the guidelines make clear there is no minimum percentage required and directs the Examining corp not to focus on numbers.

^{4/} To the extent the Examiner maintains Applicants' statements at specification page 29, lines 10-17 are too vague, they will promptly file a Declaration under Rule 132 explicitly stating "HP01263 has sufficient homology with known proteins that those of ordinary skill expect it to exhibit proteinase inhibitor activity", if such will be helpful to the Examiner. Alternatively, the Examiner can take this representation as being made by authorization. Clarification in this regard is respectfully requested.

matter of the claims will] hybridize under highly stringent conditions to known sequences because such conditions dictate that all species within the genus will be structurally similar.” Enzo Biochem v. Gen-Probe, Appeal No. 01-1230 slip op. granting reh’g at 15 (Fed. Cir. July 15, 2002).

See for instance, in In re Folkers, 145 USPQ 390 (CCPA 1965), where a new compound belonging to the known family of quinones and hydroquinones was alleged, without more, to have the electron transport activity of that known class. *Id.* at 393. The predecessor court to the Federal Circuit held that function is inferred based on similarity to a substance with a known function. *Id.* Similarly, in In re Brana 34 USPQ 1436, 1442 (Fed. Cir. 1995), the Federal Circuit noted

“[a]lthough it is true that minor changes in chemical compounds can radically alter their effects on the human body, evidence of success in structurally similar compounds is relevant in determining whether one skilled in the art would believe an asserted utility.”

Applicants wish to point out that, at the very least, the resemblance of the present invention to specific proteins of known activity makes it clear the present invention can be further utilized as research tools for better characterizing those prior art compounds. Regarding this point, that asserted utility, e.g., to better characterize prior art proteinase inhibitors, is specific. That is, while specific utility excludes generalized research tools like probes, such is not so, however, when the target being probed for is already known. Revised Interim Utility Guidelines Training Materials at 50-53.^{5/}

^{5/} In this regard, the PTO decided long ago that the ESTs must be rejected since use as research tools is not specific and they have insufficient homology to support a specific, substantial and credible utility. However, such logic (used in the context
(continued...))

Accordingly, respectfully submitted, the rejection under 35 U.S.C. § 101 is overcome and withdrawal thereof is earnestly solicited.

All claims are also rejected under 35 U.S.C. §112 first paragraph. In support of this rejection, the Examiner states that because the invention is not supported by a substantial asserted utility, one of ordinary skill would not know how to use it. However, as seen explained above, the present invention is supported by a specific and substantial utility.

Claim 12, 25 and 26 stand rejected under 35 U.S.C. §112 as failing to be adequately described in the specification as filed. In response, those claims are amended in order to address the Examiner's concerns.

Claim 14 stands rejected under 35 U.S.C. §112 as indefinite. In response, that claim is cancelled.

Claim 13 stands rejected under 35 U.S.C. §102 as anticipated for the reason noted. This rejection is plainly based on a misunderstanding of the language therein; claim 13 idiomatically recites a molecule that is complementary to the nucleic acid molecule of claims 7 or 9, not which is complementary to a portion of such. Since Hillier teaches only a fragment, such is not complementary to the entire nucleic acid molecule of the antecedent claims.

^{2/} (...continued)
of ESTs) does not extend to full-length homology-based sequences if the homologous prior art sequence has a known function, since their use as research tools is plainly specific to the homologous prior art sequence. See the Federal Circuit Bar Journal, Vol. 11, No. 4 (2002) 918.

In view of the above amendments and remarks, Applicants submit that all of the Examiner's concerns are now overcome and the claims are now in allowable condition. Accordingly, reconsideration and allowance of this application is earnestly solicited.

Claims 7, 9, 12, 13, 15-19, 21, 22, 25 and 26 remain presented for continued prosecution.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Lawrence S. Perry", is written over a horizontal line.

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